

AMENDMENTS TO THE CLAIMS

Please amend claims 24 and 25, and add new claims 33-51, as set forth below. Please withdraw claims 1-23 and 26-32, without prejudice or disclaimer.

The current listing of claims replaces all prior listings.

1. (Withdrawn) A series of isolated polynucleotides comprising at least ten polynucleotides selected from the group consisting of:

- a) a fragment of at least 20 contiguous nucleotides of a bovine genome, or
- b) a complement of a);

wherein each of the isolated polynucleotides of a), and b), comprises a nucleotide occurrence of a single nucleotide polymorphism (SNP) associated with a trait, wherein each SNP is about 500,000 or less nucleotides from position 300 of any one of SEQ ID NOS:19473 to 21982, and wherein each of the isolated polynucleotides is less than or equal to about 500,000 nucleotides in length.

2. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each SNP corresponds to a position that is about 100,000 or less nucleotides from position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.

3. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each SNP corresponds to a position that is about 10,000 or less nucleotides from position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.

4. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each SNP corresponds to a position that is within a sequence selected from of SEQ ID NOS:24493 to 64886.

5. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each SNP corresponds to position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.

6. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each polynucleotide comprises 50 contiguous nucleotides of a sequence selected from SEQ ID NOS:24493 to 64886.
7. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each polynucleotide comprises 100 contiguous nucleotides of a sequence selected from SEQ ID NOS:24493 to 64886.
8. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each polynucleotide comprises 50 contiguous nucleotides of a sequence selected from SEQ ID NOS:19473 to 21982.
9. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each polynucleotide comprises 100 contiguous nucleotides of a sequence selected from SEQ ID NOS:19473 to 21982.
10. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein each polynucleotide further comprises a detectable label at a position corresponding to position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.
11. (Withdrawn) A series of at least ten oligonucleotides that each bind to a different sequence selected from SEQ ID NOS:19473 to 21982, wherein each oligonucleotide is between 10 and 50 nucleotides in length, and wherein each oligonucleotide comprises at least 10 contiguous nucleotides of a sequence selected from SEQ ID NOS:21983 to 24492.
12. (Withdrawn) The series of oligonucleotides of claim 11, wherein each oligonucleotide is at least 15 nucleotides in length.
13. (Withdrawn) The series of oligonucleotides of claim 12, wherein each oligonucleotide binds to a region that comprises position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.

14. (Withdrawn) The series of oligonucleotides of claim 12, wherein each oligonucleotide comprises at least 15 nucleotides of a sequence selected from SEQ ID NOS:21983 to 24492.

15. (Withdrawn) The series of oligonucleotides of claim 12, wherein each oligonucleotide is a sequence selected from SEQ ID NOS:21983 to 24492.

16. (Withdrawn) A series of at least ten primer pairs, wherein each primer pair comprises a first primer that binds to a first target region of a sequence selected from SEQ ID NOS:24493 to 64886 and a second primer that binds to the complement of a second target region of the sequence, wherein the a first primer rand the second primer of each primer pair are at least 10 nucleotides in length, and prime polynucleotide synthesis from the first and second target regions in opposite directions across position 300 of a sequence selected SEQ ID NOS:19473 to 21982.

17. (Withdrawn) The series of primer pairs of claim 16, wherein each primer pair binds to a region within a sequence selected from SEQ ID NOS:19473 to 21982.

18. (Withdrawn) A series of at least ten isolated oligonucleotides, wherein each isolated oligonucleotide selectively binds to a target polynucleotide of SEQ ID NOS:19473 to 21982, wherein a terminal nucleotide of each of the isolated oligonucleotides binds to position 299, 300, or 301 of a sequence selected from SEQ ID NOS:19473 to 21982.

19. (Withdrawn) The series of isolated oligonucleotides of claim 18, wherein each oligonucleotide is at least 15 nucleotides in length.

20. (Withdrawn) The series of isolated oligonucleotides of claim 18, wherein the terminal nucleotide of each oligonucleotide binds to position 300 of a sequence selected from SEQ ID NOS:19473 to 21982.

21. (Withdrawn) A series of at least ten isolated oligonucleotide pairs, wherein each pair is effective for determining a nucleotide occurrence at a single nucleotide polymorphism (SNP) corresponding to position 300 of a sequence selected from SEQ ID NOS:19473 to 21982, wherein each isolated oligonucleotide comprises at least 5 nucleotides from the sequence selected from SEQ ID NOS:19473 to 21982 and wherein the terminal nucleotide of each oligonucleotide of the pair is complementary to a different nucleotide at position 300 of the sequence selected from SEQ ID NOS:19473 to 21982 or a complement thereof.
22. (Withdrawn) An isolated vector comprising at least one of the series of polynucleotides of claim 1.
23. (Withdrawn) An isolated cell comprising the vector of claim 22.
24. (Currently Amended) A ~~series of~~ combination of isolated polynucleotides comprising:
- a) a first and second primer each of which binds to a first strand of a target sequence on bovine genomic DNA, wherein the DNA comprises a SNP position associated with a bovine trait, and wherein each primer comprises at least 20 contiguous nucleotides which are at least 90% identical to the sequences upstream and adjacent to the SNP position, wherein the first or second primer comprises a residue which is complementary to a specific sequence variant which comprises the SNP position; or
 - b) complements of the first and second primers; and
 - c) an extension primer which binds to the first and second strand of the target sequence downstream from the primers of (a) or (b), wherein the extension primer is a substrate for polynucleotide synthesis across the SNP position, and wherein the SNP position corresponds to nucleic acid residue 300 of SEQ ID NO:20614
~~at least ten polynucleotides selected from the group consisting of:~~

~~a) a polynucleotide that is at least 20 nucleotides in length and is at least 90% identical to a fragment of at least 20 contiguous nucleotides of a bovine genome; or~~

~~b) a complement of a);~~

~~wherein the fragment of at least 20 contiguous nucleotides of the bovine genome comprises a nucleotide occurrence of a single nucleotide polymorphism (SNP) that corresponds to position 300 of any one of SEQ ID NOS:19473 to 21982.~~

25. (Currently Amended) The combination series of isolated polynucleotides of claim 24, wherein each isolated polynucleotide is at least 25 nucleotides in length.

26. (Withdrawn) The series of isolated polynucleotides of claim 24, wherein each isolated polynucleotide is at least 90% identical to a fragment of at least 20 contiguous nucleotides of any one of a series of at least ten sequences selected from the group consisting of SEQ ID NOS:19473 to 21982.

27. (Withdrawn) The series of isolated polynucleotides of claim 1, wherein the series comprises at least 100 polynucleotides.

28. (Withdrawn) The series of oligonucleotides of claim 11, wherein the series comprises at least 100 polynucleotides.

29. (Withdrawn) The series of primer pairs of claim 16, wherein the primers of each pair bind to a first target region and a second target region of one of a series comprising at least 100 sequences selected from SEQ ID NOS:24493 to 64886.

30. (Withdrawn) The series of isolated oligonucleotides of claim 18, wherein each oligonucleotide selectively binds to a target polynucleotide of a series of at least 100 sequences selected from SEQ ID NOS:19473 to 21982.

31. (Withdrawn) The series of isolated oligonucleotide pairs of claim 21, wherein each pair is effective for determining a nucleotide occurrence at a single nucleotide polymorphism (SNP) corresponding to position 300 of a series of at least 100 sequences selected from SEQ ID NOS:19473 to 21982.

32. (Withdrawn) The series of isolated polynucleotides of claim 24, wherein the series comprises at least 100 polynucleotides.

33. (New) The combination of isolated polynucleotides of claim 24, wherein the target sequence is DNA or RNA.

34. (New) The combination of isolated polynucleotides of claim 24, wherein a nucleotide occurrence for the SNP position is associated with a value of at least a 50th percentile of the bovine population for the trait.

35. (New) The combination of isolated polynucleotides of claim 34, wherein a nucleotide occurrence for the SNP position is associated with a value of at least a 99th percentile of the bovine population for the trait.

36. (New) The combination of isolated polynucleotides of claim 24, wherein the associated bovine trait is tenderness.

37. (New) The combination of isolated polynucleotides of claim 36, wherein the SNP is in linkage disequilibrium with one or more markers for the same trait within a distance of about 500,000 nucleotides on either side of nucleic acid residue 300 of SEQ ID NO:20614.

38. (New) The combination of isolated polynucleotides of claim 36, wherein the SNP is in linkage disequilibrium with one or more markers for the same trait within a distance of about 100,000 nucleotides on either side of nucleic acid residue 300 of SEQ ID NO:20614.

39. (New) The combination of isolated polynucleotides of claim 36, wherein the SNP is in linkage disequilibrium with one or more markers for the same trait within a distance of about 10,000 nucleotides on either side of nucleic acid residue 300 of SEQ ID NO:20614.

40. (New) The combination of isolated polynucleotides of claim 24, wherein at least one of the first and second primers comprises non-target sequences.

41. (New) The combination of isolated polynucleotides of claim 24, wherein at least one of the first and second primers is bound to a solid phase.

42. (New) The combination of isolated polynucleotides of claim 24, wherein at least one of the first and second primers is detectably labeled.

43. (New) The combination of isolated polynucleotides of claim 42, wherein the detectable label is at a position corresponding to position 300 of SEQ ID NO:20614.

44. (New) The combination of isolated polynucleotides of claim 40, wherein at least one of the first and second primers comprises a target sequence for a separate third primer.

45. (New) The combination of isolated polynucleotides of claim 24, wherein the extension primer comprises at least 20 contiguous nucleotides which are at least 90% identical to the sequences upstream and adjacent to the SNP position, and wherein the extension primer comprises a 3'-terminal residue which is at least one nucleotide position upstream from position 300 of sequence SEQ ID NO:20614.

46. (New) The combination of isolated polynucleotides of claim 45, wherein the extension primer binds to the same strand as the first or second primer.

47. (New) The combination of isolated polynucleotides of claim 24, wherein the extension primer binds to a different strand from the first or second primer.

48. (New) The combination of isolated polynucleotides of claim 24, wherein the extension primer is detectably labeled.

49. (New) The combination of isolated poly nucleotides of claim 24, wherein the extension primer comprises non-target sequences.

50. (New) The combination of isolated polynucleotides of claim 49, wherein the extension primer comprises a target sequence for a separate third primer.

51. (New) The combination of isolated polynucleotides of claim 24, wherein at least one of the primers comprises a 3'-terminal nucleotide residue which is complementary to a specific sequence variant which comprises the SNP position.